

## SEQUENCE LISTING

&lt;110&gt; Acton, Susan L. et al.

<120> ANGIOTENSIN CONVERTING ENZYME HOMOLOG AND THERAPEUTIC  
DIAGNOSTIC USES THEREFOR

&lt;130&gt; MNI-132CP

&lt;140&gt; 09/163,648

&lt;141&gt; 1998-09-30

&lt;150&gt; 08/989,299

&lt;151&gt; 1997-12-11

&lt;160&gt; 24

&lt;170&gt; PatentIn Ver. 2.0

&lt;210&gt; 1

&lt;211&gt; 3396

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (82)..(2496)

&lt;400&gt; 1

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Pro Leu Tyr Glu His Leu His Ala Tyr Val Arg Ala Lys Leu Met Asn	
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Ala Tyr Pro Ser Tyr Ile Ser Pro Ile Gly Cys Leu Pro Ala His Leu	
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Lys Val Thr Met Asp Asp Phe Leu Thr Ala His His Glu Met Gly His	
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Ile Gln Tyr Asp Met Ala Tyr Ala Ala Gln Pro Phe Leu Leu Arg Asn	
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&lt;210&gt; 2

&lt;211&gt; 805

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2

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	50					55					60				
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Gln	Met	Tyr	Pro	Leu	Gln	Glu	Ile	Gln	Asn	Leu	Thr	Val	Lys	Leu	Gln
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Ser	Lys	Arg	Leu	Asn	Thr	Ile	Leu	Asn	Thr	Met	Ser	Thr	Ile	Tyr	Ser
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 Val Asn Gly Val Asp Gly Tyr Asp Tyr Ser Arg Gly Gln Leu Ile Glu  
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 Asp Val Glu His Thr Phe Glu Glu Ile Lys Pro Leu Tyr Glu His Leu  
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 His Ala Tyr Val Arg Ala Lys Leu Met Asn Ala Tyr Pro Ser Tyr Ile  
 245 250 255  
 Ser Pro Ile Gly Cys Leu Pro Ala His Leu Leu Gly Asp Met Trp Gly  
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 Lys Gly Asp Phe Arg Ile Leu Met Cys Thr Lys Val Thr Met Asp Asp  
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 Phe Leu Thr Ala His His Glu Met Gly His Ile Gln Tyr Asp Met Ala  
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 Tyr Ala Ala Gln Pro Phe Leu Leu Arg Asn Gly Ala Asn Glu Gly Phe  
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 His Glu Ala Val Gly Glu Ile Met Ser Leu Ser Ala Ala Thr Pro Lys  
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 His Leu Lys Ser Ile Gly Leu Leu Ser Pro Asp Phe Gln Glu Asp Asn  
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 Glu Thr Glu Ile Asn Phe Leu Leu Lys Gln Ala Leu Thr Ile Val Gly  
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<213> Homo sapiens

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&lt;210&gt; 4

&lt;211&gt; 732

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 4

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Ser	Pro	Asn	Leu	Val	Thr	Asp	Glu	Ala	Glu	Ala	Ser	Lys	Phe	Val	Glu
		65			70				75						80
Glu	Tyr	Asp	Arg	Thr	Ser	Gln	Val	Val	Trp	Asn	Glu	Tyr	Ala	Glu	Ala
			85					90						95	
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		130				135					140				

Arg Ile Ile Lys Lys Val Gln Asp Leu Glu Arg Ala Ala Leu Pro Ala  
 145 150 155 160  
 Gln Glu Leu Glu Glu Tyr Asn Lys Ile Leu Leu Asp Met Glu Thr Thr  
 165 170 175  
 Tyr Ser Val Ala Thr Val Cys His Pro Asn Gly Ser Cys Leu Gln Leu  
 180 185 190  
 Glu Pro Asp Leu Thr Asn Val Met Ala Thr Ser Arg Lys Tyr Glu Asp  
 195 200 205  
 Leu Leu Trp Ala Trp Glu Gly Trp Arg Asp Lys Ala Gly Arg Ala Ile  
 210 215 220  
 Leu Gln Phe Tyr Pro Lys Tyr Val Glu Leu Ile Asn Gln Ala Ala Arg  
 225 230 235 240  
 Leu Asn Gly Tyr Val Asp Ala Gly Asp Ser Trp Arg Ser Met Tyr Glu  
 245 250 255  
 Thr Pro Ser Leu Glu Gln Asp Leu Glu Arg Leu Phe Gln Glu Leu Gln  
 260 265 270  
 Pro Leu Tyr Leu Asn Leu His Ala Tyr Val Arg Arg Ala Leu His Arg  
 275 280 285  
 His Tyr Gly Ala Gln His Ile Asn Leu Glu Gly Pro Ile Pro Ala His  
 290 295 300  
 Leu Leu Gly Asn Met Trp Ala Gln Thr Trp Ser Asn Ile Tyr Asp Leu  
 305 310 315 320  
 Val Val Pro Phe Pro Ser Ala Pro Ser Met Asp Thr Thr Glu Ala Met  
 325 330 335  
 Leu Lys Gln Gly Trp Thr Pro Arg Arg Met Phe Lys Glu Ala Asp Asp  
 340 345 350  
 Phe Phe Thr Ser Leu Gly Leu Leu Pro Val Pro Pro Glu Phe Trp Asn  
 355 360 365  
 Lys Ser Met Leu Glu Lys Pro Thr Asp Gly Arg Glu Val Val Cys His  
 370 375 380  
 Ala Ser Ala Trp Asp Phe Tyr Asn Gly Lys Asp Phe Arg Ile Lys Gln  
 385 390 395 400  
 Cys Thr Thr Val Asn Leu Glu Asp Leu Val Val Ala His His Glu Met  
 405 410 415  
 Gly His Ile Gln Tyr Phe Met Gln Tyr Lys Asp Leu Pro Val Ala Leu  
 420 425 430  
 Arg Glu Gly Ala Asn Pro Gly Phe His Glu Ala Ile Gly Asp Val Leu  
 435 440 445  
 Ala Leu Ser Val Ser Thr Pro Lys His Leu His Ser Leu Asn Leu Leu  
 450 455 460

Ser Ser Glu Gly Gly Ser Asp Glu His Asp Ile Asn Phe Leu Met Lys  
 465 470 475 480  
 Met Ala Leu Asp Lys Ile Ala Phe Ile Pro Phe Ser Tyr Leu Val Asp  
 485 490 495  
 Gln Trp Arg Trp Arg Val Phe Asp Gly Ser Ile Thr Lys Glu Asn Tyr  
 500 505 510  
 Asn Gln Glu Trp Trp Ser Leu Arg Leu Lys Tyr Gln Gly Leu Cys Pro  
 515 520 525  
 Pro Val Pro Arg Thr Gln Gly Asp Phe Asp Pro Gly Ala Lys Phe His  
 530 535 540  
 Ile Pro Ser Ser Val Pro Tyr Ile Arg Tyr Phe Val Ser Phe Ile Ile  
 545 550 555 560  
 Gln Phe Gln Phe His Glu Ala Leu Cys Gln Ala Ala Gly His Thr Gly  
 565 570 575  
 Pro Leu His Lys Cys Asp Ile Tyr Gln Ser Lys Glu Ala Gly Gln Arg  
 580 585 590  
 Leu Ala Thr Ala Met Lys Leu Gly Phe Ser Arg Pro Trp Pro Glu Ala  
 595 600 605  
 Met Gln Leu Ile Thr Gly Gln Pro Asn Met Ser Ala Ser Ala Met Leu  
 610 615 620  
 Ser Tyr Phe Lys Pro Leu Leu Asp Trp Leu Arg Thr Glu Asn Glu Leu  
 625 630 635 640  
 His Gly Glu Lys Leu Gly Trp Pro Gln Tyr Asn Trp Thr Pro Asn Ser  
 645 650 655  
 Ala Arg Ser Glu Gly Pro Leu Pro Asp Ser Gly Arg Val Ser Phe Leu  
 660 665 670  
 Gly Leu Asp Leu Asp Ala Gln Gln Ala Arg Val Gly Gln Trp Leu Leu  
 675 680 685  
 Leu Phe Leu Gly Ile Ala Leu Leu Val Ala Thr Leu Gly Leu Ser Gln  
 690 695 700  
 Arg Leu Phe Ser Ile Arg His Arg Ser Leu His Arg His Ser His Gly  
 705 710 715 720  
 Pro Gln Phe Gly Ser Glu Val Glu Leu Arg His Ser  
 725 730

&lt;210&gt; 5

&lt;211&gt; 732

&lt;212&gt; PRT

&lt;213&gt; Murine sp.

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: motifs

&lt;400&gt; 5

Met Gly Gln Gly Trp Ala Thr Pro Gly Leu Pro Ser Phe Leu Phe Leu  
 1 5 10 15  
 Leu Leu Cys Cys Gly His His Leu Leu Val Leu Ser Gln Val Ala Thr  
 20 25 30  
 Asp His Val Thr Ala Asn Gln Gly Ile Thr Asn Gln Ala Thr Thr Arg  
 35 40 45  
 Ser Gln Thr Thr Thr His Gln Ala Thr Ile Asp Gln Thr Thr Gln Ile  
 50 55 60  
 Pro Asn Leu Glu Thr Asp Glu Ala Lys Ala Asp Arg Phe Val Glu Glu  
 65 70 75 80  
 Tyr Asp Arg Thr Ala Gln Val Leu Leu Asn Glu Tyr Ala Glu Ala Asn  
 85 90 95  
 Trp Gln Tyr Asn Thr Asn Ile Thr Ile Glu Gly Ser Lys Ile Leu Leu  
 100 105 110  
 Glu Lys Ser Thr Glu Val Ser Asn His Thr Leu Lys Tyr Gly Thr Arg  
 115 120 125  
 Ala Lys Thr Phe Asp Val Ser Asn Phe Gln Asn Ser Ser Ile Lys Arg  
 130 135 140  
 Ile Ile Lys Lys Leu Gln Asn Leu Asp Arg Ala Val Leu Pro Pro Lys  
 145 150 155 160  
 Glu Leu Glu Glu Tyr Asn Gln Ile Leu Leu Asp Met Glu Thr Thr Tyr  
 165 170 175  
 Ser Leu Ser Asn Ile Cys Tyr Thr Asn Gly Thr Cys Met Pro Leu Glu  
 180 185 190  
 Pro Asp Leu Thr Asn Met Met Ala Thr Ser Arg Lys Tyr Glu Glu Leu  
 195 200 205  
 Leu Trp Ala Trp Lys Ser Trp Arg Asp Lys Val Gly Arg Ala Ile Leu  
 210 215 220  
 Pro Phe Phe Pro Lys Tyr Val Glu Phe Ser Asn Lys Ile Ala Lys Leu  
 225 230 235 240  
 Asn Gly Tyr Thr Asp Ala Gly Asp Ser Trp Arg Ser Leu Tyr Glu Ser  
 245 250 255  
 Asp Asn Leu Glu Gln Asp Leu Glu Lys Leu Tyr Gln Glu Leu Gln Pro  
 260 265 270  
 Leu Tyr Leu Asn Leu His Ala Tyr Val Arg Arg Ser Leu His Arg His  
 275 280 285  
 Tyr Gly Ser Glu Tyr Ile Asn Leu Asp Gly Pro Ile Pro Ala His Leu  
 290 295 300  
 Leu Gly Asn Met Trp Ala Gln Thr Trp Ser Asn Ile Tyr Asp Leu Val  
 305 310 315 320

Ala Pro Phe Pro Ser Ala Pro Asn Ile Asp Ala Thr Glu Ala Met Ile  
 325 330 335  
 Lys Gln Gly Trp Thr Pro Arg Arg Ile Phe Lys Glu Ala Asp Asn Phe  
 340 345 350  
 Phe Thr Ser Leu Gly Leu Leu Pro Val Pro Pro Glu Phe Trp Asn Lys  
 355 360 365  
 Ser Met Leu Glu Lys Pro Thr Asp Gly Arg Glu Val Val Cys His Pro  
 370 375 380  
 Ser Ala Trp Asp Phe Tyr Asn Gly Lys Asp Phe Arg Ile Lys Gln Cys  
 385 390 395 400  
 Thr Ser Val Asn Met Glu Asp Leu Val Ile Ala His His Glu Met Gly  
 405 410 415  
 His Ile Gln Tyr Phe Met Gln Tyr Lys Asp Leu Pro Val Thr Phe Arg  
 420 425 430  
 Glu Gly Ala Asn Pro Gly Phe His Glu Ala Ile Gly Asp Ile Met Ala  
 435 440 445  
 Leu Ser Val Ser Thr Pro Lys His Leu Tyr Ser Leu Asn Leu Leu Ser  
 450 455 460  
 Thr Glu Gly Ser Gly Tyr Glu Tyr Asp Ile Asn Phe Leu Met Lys Met  
 465 470 475 480  
 Ala Leu Asp Lys Ile Ala Phe Ile Pro Phe Ser Tyr Leu Ile Asp Gln  
 485 490 495  
 Trp Arg Trp Arg Val Phe Asp Gly Ser Ile Thr Lys Glu Asn Tyr Asn  
 500 505 510  
 Gln Glu Trp Trp Ser Leu Arg Leu Lys Tyr Gln Gly Leu Cys Pro Pro  
 515 520 525  
 Val Pro Arg Ser Gln Gly Asp Phe Asp Pro Gly Ser Lys Phe His Val  
 530 535 540  
 Pro Ala Asn Val Pro Tyr Val Arg Tyr Phe Val Ser Phe Ile Ile Gln  
 545 550 555 560  
 Phe Gln Phe His Glu Ala Leu Cys Arg Ala Ala Gly His Thr Gly Pro  
 565 570 575  
 Leu His Lys Cys Asp Ile Tyr Gln Ser Lys Glu Ala Gly Lys Leu Leu  
 580 585 590  
 Ala Asp Ala Met Lys Leu Gly Tyr Ser Lys Pro Trp Pro Glu Ala Met  
 595 600 605  
 Lys Leu Ile Thr Gly Gln Pro Asn Met Ser Ala Ser Ala Met Met Asn  
 610 615 620  
 Tyr Phe Lys Pro Leu Thr Glu Trp Leu Val Thr Glu Asn Arg Arg His  
 625 630 635 640

Gly Glu Thr Leu Gly Trp Pro Glu Tyr Asn Trp Ala Pro Asn Thr Ala  
                     645                    650                    655  
 Arg Ala Glu Gly Ser Thr Ala Glu Ser Asn Arg Val Asn Phe Leu Gly  
                     660                    665                    670  
 Leu Tyr Leu Glu Pro Gln Gln Ala Arg Val Gly Gln Trp Val Leu Leu  
                     675                    680                    685  
 Phe Leu Gly Val Ala Leu Leu Val Ala Thr Val Gly Leu Ala His Arg  
                     690                    695                    700  
 Leu Tyr Asn Ile Arg Asn His His Ser Leu Arg Arg Pro His Arg Gly  
 705                    710                    715                    720  
 Pro Gln Phe Gly Ser Glu Val Glu Leu Arg His Ser  
                     725                    730

&lt;210&gt; 6

&lt;211&gt; 737

&lt;212&gt; PRT

<213> *Oryctolagus cuniculus*

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: motifs

&lt;400&gt; 6

Met Gly Gln Gly Trp Ala Ala Pro Gly Leu Pro Ser Leu Leu Leu Leu  
   1                    5                    10                    15  
 Leu Leu Cys Cys Gly His Ser Leu Leu Val Pro Ser Arg Val Ala Ala  
                     20                    25                    30  
 Arg Arg Val Thr Val Asn Gln Gly Thr Thr Ser Gln Ala Thr Thr Thr  
                     35                    40                    45  
 Ser Lys Ala Thr Thr Ser Ile Arg Ala Thr Thr His Gln Thr Thr Ala  
                     50                    55                    60  
 His Gln Thr Thr Gln Ser Pro Asn Leu Val Thr Asp Glu Ala Glu Ala  
                     65                    70                    75                    80  
 Ser Arg Phe Val Glu Glu Tyr Asp Arg Ser Phe Gln Ala Val Trp Asn  
                     85                    90                    95  
 Glu Tyr Ala Glu Ala Asn Trp Asn Tyr Asn Thr Asn Ile Thr Thr Glu  
                     100                    105                    110  
 Ala Ser Lys Ile Leu Leu Gln Lys Asn Met Gln Ile Ala Asn His Thr  
                     115                    120                    125  
 Leu Thr Tyr Gly Asn Trp Ala Arg Arg Phe Asp Val Ser Asn Phe Gln  
                     130                    135                    140  
 Asn Ala Thr Ser Lys Arg Ile Ile Lys Lys Val Gln Asp Leu Gln Arg  
                     145                    150                    155                    160  
 Ala Val Leu Pro Val Lys Glu Leu Glu Glu Tyr Asn Gln Ile Leu Leu  
                     165                    170                    175

Asp	Met	Glu	Thr	Ile	Tyr	Ser	Val	Ala	Asn	Val	Cys	Arg	Val	Asp	Gly	180	185	190
Ser	Cys	Leu	Gln	Leu	Glu	Pro	Asp	Leu	Thr	Asn	Leu	Met	Ala	Thr	Ser	195	200	205
Arg	Lys	Tyr	Asp	Glu	Leu	Leu	Trp	Val	Trp	Thr	Ser	Trp	Arg	Asp	Lys	210	215	220
Val	Gly	Arg	Ala	Ile	Leu	Pro	Tyr	Phe	Pro	Lys	Tyr	Val	Glu	Phe	Thr	225	230	235
Asn	Lys	Ala	Ala	Arg	Leu	Asn	Gly	Tyr	Val	Asp	Ala	Gly	Asp	Ser	Trp	245	250	255
Arg	Ser	Met	Tyr	Glu	Thr	Pro	Thr	Leu	Glu	Gln	Asp	Leu	Glu	Arg	Leu	260	265	270
Phe	Gln	Glu	Leu	Gln	Pro	Leu	Tyr	Leu	Asn	Leu	His	Ala	Tyr	Val	Gly	275	280	285
Arg	Ala	Leu	His	Arg	His	Tyr	Gly	Ala	Gln	His	Ile	Asn	Leu	Glu	Gly	290	295	300
Pro	Ile	Pro	Ala	His	Leu	Leu	Gly	Asn	Met	Trp	Ala	Gln	Thr	Trp	Ser	305	310	315
Asn	Ile	Tyr	Asp	Leu	Val	Ala	Pro	Phe	Pro	Ser	Ala	Ser	Thr	Met	Asp	325	330	335
Ala	Thr	Glu	Ala	Met	Ile	Lys	Gln	Gly	Trp	Thr	Pro	Arg	Arg	Met	Phe	340	345	350
Glu	Glu	Ala	Asp	Lys	Phe	Phe	Ile	Ser	Leu	Gly	Leu	Leu	Pro	Val	Pro	355	360	365
Pro	Glu	Phe	Trp	Asn	Lys	Ser	Met	Leu	Glu	Lys	Pro	Thr	Asp	Gly	Arg	370	375	380
Glu	Val	Val	Cys	His	Ala	Ser	Ala	Trp	Asp	Phe	Tyr	Asn	Gly	Lys	Asp	385	390	395
Phe	Arg	Ile	Lys	Gln	Cys	Thr	Thr	Val	Asn	Met	Glu	Asp	Leu	Val	Val	405	410	415
Val	His	His	Glu	Met	Gly	His	Ile	Gln	Tyr	Phe	Met	Gln	Tyr	Lys	Asp	420	425	430
Leu	Pro	Val	Ala	Leu	Arg	Glu	Gly	Ala	Asn	Pro	Gly	Phe	His	Glu	Ala	435	440	445
Ile	Gly	Asp	Val	Leu	Ala	Leu	Ser	Val	Ser	Thr	Pro	Lys	His	Leu	His	450	455	460
Ser	Ile	Asn	Leu	Leu	Ser	Ser	Glu	Gly	Gly	Gly	Tyr	Glu	His	Asp	Ile	465	470	475
Asn	Phe	Leu	Met	Lys	Met	Ala	Leu	Asp	Lys	Ile	Ala	Phe	Ile	Pro	Phe	485	490	495

Ser Tyr Leu Val Asp Glu Trp Arg Trp Arg Val Phe Asp Gly Ser Ile  
 500 505 510  
 Thr Lys Glu Asn Tyr Asn Gln Glu Trp Trp Ser Leu Arg Leu Lys Tyr  
 515 520 525  
 Gln Gly Leu Cys Pro Pro Ala Pro Arg Ser Gln Gly Asp Phe Asp Pro  
 530 535 540  
 Gly Ala Lys Phe His Ile Pro Ser Ser Val Pro Tyr Ile Arg Tyr Phe  
 545 550 555 560  
 Val Ser Phe Ile Ile Gln Phe Gln Phe His Glu Ala Leu Cys Lys Ala  
 565 570 575  
 Ala Gly His Thr Gly Pro Leu His Thr Cys Asp Ile Tyr Gln Ser Lys  
 580 585 590  
 Glu Ala Gly Lys Arg Leu Ala Asp Ala Met Lys Leu Gly Tyr Ser Lys  
 595 600 605  
 Pro Trp Pro Glu Ala Met Lys Val Ile Thr Gly Gln Pro Asn Met Ser  
 610 615 620  
 Ala Ser Ala Met Met Asn Tyr Phe Lys Pro Leu Met Asp Trp Leu Leu  
 625 630 635 640  
 Thr Glu Asn Gly Arg His Gly Glu Lys Leu Gly Trp Pro Gln Tyr Thr  
 645 650 655  
 Trp Thr Pro Asn Ser Ala Arg Ser Glu Gly Ser Leu Pro Asp Ser Gly  
 660 665 670  
 Arg Val Asn Phe Leu Gly Met Asn Leu Asp Ala Gln Gln Ala Arg Val  
 675 680 685  
 Gly Gln Trp Val Leu Leu Phe Leu Gly Val Ala Leu Leu Leu Ala Ser  
 690 695 700  
 Leu Gly Leu Thr Gln Arg Leu Phe Ser Ile Arg Tyr Gln Ser Leu Arg  
 705 710 715 720  
 Gln Pro His His Gly Pro Gln Phe Gly Ser Glu Val Glu Leu Arg His  
 725 730 735

Ser

<210> 7

<211> 1306

<212> PRT

<213> Homo sapiens

<220>

<223> Description of Artificial Sequence: motifs

<400> 7

Met Gly Ala Ala Ser Gly Arg Arg Gly Pro Gly Leu Leu Leu Pro Leu  
 1 5 10 15



Pro Leu Leu Leu Leu Leu Pro Pro Gln Pro Ala Leu Ala Leu Asp Pro  
 20 25 30  
 Gly Leu Gln Pro Gly Asn Phe Ser Ala Asp Glu Ala Gly Ala Gln Leu  
 35 40 45  
 Phe Ala Gln Ser Tyr Asn Ser Ser Ala Glu Gln Val Leu Phe Gln Ser  
 50 55 60  
 Val Ala Ala Ser Trp Ala His Asp Thr Asn Ile Thr Ala Glu Asn Ala  
 65 70 75 80  
 Arg Arg Gln Glu Glu Ala Ala Leu Leu Ser Gln Glu Phe Ala Glu Ala  
 85 90 95  
 Trp Gly Gln Lys Ala Lys Glu Leu Tyr Glu Pro Ile Trp Gln Asn Phe  
 100 105 110  
 Thr Asp Pro Gln Leu Arg Arg Ile Ile Gly Ala Val Arg Thr Leu Gly  
 115 120 125  
 Ser Ala Asn Leu Pro Leu Ala Lys Arg Gln Gln Tyr Asn Ala Leu Leu  
 130 135 140  
 Ser Asn Met Ser Arg Ile Tyr Ser Thr Ala Lys Val Cys Leu Pro Asn  
 145 150 155 160  
 Lys Thr Ala Thr Cys Trp Ser Leu Asp Pro Asp Leu Thr Asn Ile Leu  
 165 170 175  
 Ala Ser Ser Arg Ser Tyr Ala Met Leu Leu Phe Ala Trp Glu Gly Trp  
 180 185 190  
 His Asn Ala Ala Gly Ile Pro Leu Lys Pro Leu Tyr Glu Asp Phe Thr  
 195 200 205  
 Ala Leu Ser Asn Glu Ala Tyr Lys Gln Asp Gly Phe Thr Asp Thr Gly  
 210 215 220  
 Ala Tyr Trp Arg Ser Trp Tyr Asn Ser Pro Thr Phe Glu Asp Asp Leu  
 225 230 235 240  
 Glu His Leu Tyr Gln Gln Leu Glu Pro Leu Tyr Leu Asn Leu His Ala  
 245 250 255  
 Phe Val Arg Arg Ala Leu His Arg Arg Tyr Gly Asp Arg Tyr Ile Asn  
 260 265 270  
 Leu Arg Gly Pro Ile Pro Ala His Leu Leu Gly Asp Met Trp Ala Gln  
 275 280 285  
 Ser Trp Glu Asn Ile Tyr Asp Met Val Val Pro Phe Pro Asp Lys Pro  
 290 295 300  
 Asn Leu Asp Val Thr Ser Thr Met Leu Gln Gln Gly Trp Asn Ala Thr  
 305 310 315 320  
 His Met Phe Arg Val Ala Glu Glu Phe Phe Thr Ser Leu Glu Leu Ser  
 325 330 335

Pro Met Pro Pro Glu Phe Trp Glu Gly Ser Met Leu Glu Lys Pro Ala  
 340 345 350  
 Asp Gly Arg Glu Val Val Cys His Ala Ser Ala Trp Asp Phe Tyr Asn  
 355 360 365  
 Arg Lys Asp Phe Arg Ile Lys Gln Cys Thr Arg Val Thr Met Asp Gln  
 370 375 380  
 Leu Ser Thr Val His His Glu Met Gly His Ile Gln Tyr Tyr Leu Gln  
 385 390 395 400  
 Tyr Lys Asp Leu Pro Val Ser Leu Arg Arg Gly Ala Asn Pro Gly Phe  
 405 410 415  
 His Glu Ala Ile Gly Asp Val Leu Ala Leu Ser Val Ser Thr Pro Glu  
 420 425 430  
 His Leu His Lys Ile Gly Leu Leu Asp Arg Val Thr Asn Asp Thr Glu  
 435 440 445  
 Ser Asp Ile Asn Tyr Leu Leu Lys Met Ala Leu Glu Lys Ile Ala Phe  
 450 455 460  
 Leu Pro Phe Gly Tyr Leu Val Asp Gln Trp Arg Trp Gly Val Phe Ser  
 465 470 475 480  
 Gly Arg Thr Pro Pro Ser Arg Tyr Asn Phe Asp Trp Trp Tyr Leu Arg  
 485 490 495  
 Thr Lys Tyr Gln Gly Ile Cys Pro Pro Val Thr Arg Asn Glu Thr His  
 500 505 510  
 Phe Asp Ala Gly Ala Lys Phe His Val Pro Asn Val Thr Pro Tyr Ile  
 515 520 525  
 Arg Tyr Phe Val Ser Phe Val Leu Gln Phe Gln Phe His Glu Ala Leu  
 530 535 540  
 Cys Lys Glu Ala Gly Tyr Glu Gly Pro Leu His Gln Cys Asp Ile Tyr  
 545 550 555 560  
 Arg Ser Thr Lys Ala Gly Ala Lys Leu Arg Lys Val Leu Gln Ala Gly  
 565 570 575  
 Ser Ser Arg Pro Trp Gln Glu Val Leu Lys Asp Met Val Gly Leu Asp  
 580 585 590  
 Ala Leu Asp Ala Gln Pro Leu Leu Lys Tyr Phe Gln Pro Val Thr Gln  
 595 600 605  
 Trp Leu Gln Glu Gln Asn Gln Gln Asn Gly Glu Val Leu Gly Trp Pro  
 610 615 620  
 Glu Tyr Gln Trp His Pro Pro Leu Pro Asp Asn Tyr Pro Glu Gly Ile  
 625 630 635 640  
 Asp Leu Val Thr Asp Glu Ala Glu Ala Ser Lys Phe Val Glu Glu Tyr  
 645 650 655

Asp Arg Thr Ser Gln Val Val Trp Asn Glu Tyr Ala Glu Ala Asn Trp  
 660 665 670  
 Asn Tyr Asn Thr Asn Ile Thr Thr Glu Thr Ser Lys Ile Leu Leu Gln  
 675 680 685  
 Lys Asn Met Gln Ile Ala Asn His Thr Leu Lys Tyr Gly Thr Gln Ala  
 690 695 700  
 Arg Lys Phe Asp Val Asn Gln Leu Gln Asn Thr Thr Ile Lys Arg Ile  
 705 710 715 720  
 Ile Lys Lys Val Gln Asp Leu Glu Arg Ala Ala Leu Pro Ala Gln Glu  
 725 730 735  
 Leu Glu Glu Tyr Asn Lys Ile Leu Leu Asp Met Glu Thr Thr Tyr Ser  
 740 745 750  
 Val Ala Thr Val Cys His Pro Asn Gly Ser Cys Leu Gln Leu Glu Pro  
 755 760 765  
 Asp Leu Thr Asn Val Met Ala Thr Ser Arg Lys Tyr Glu Asp Leu Leu  
 770 775 780  
 Trp Ala Trp Glu Gly Trp Arg Asp Lys Ala Gly Arg Ala Ile Leu Gln  
 785 790 795 800  
 Phe Tyr Pro Lys Tyr Val Glu Leu Ile Asn Gln Ala Ala Arg Leu Asn  
 805 810 815  
 Gly Tyr Val Asp Ala Gly Asp Ser Trp Arg Ser Met Tyr Glu Thr Pro  
 820 825 830  
 Ser Leu Glu Gln Asp Leu Glu Arg Leu Phe Gln Glu Leu Gln Pro Leu  
 835 840 845  
 Tyr Leu Asn Leu His Ala Tyr Val Arg Arg Ala Leu His Arg His Tyr  
 850 855 860  
 Gly Ala Gln His Ile Asn Leu Glu Gly Pro Ile Pro Ala His Leu Leu  
 865 870 875 880  
 Gly Asn Met Trp Ala Gln Thr Trp Ser Asn Ile Tyr Asp Leu Val Val  
 885 890 895  
 Pro Phe Pro Ser Ala Pro Ser Met Asp Thr Thr Glu Ala Met Leu Lys  
 900 905 910  
 Gln Gly Trp Thr Pro Arg Arg Met Phe Lys Glu Ala Asp Asp Phe Phe  
 915 920 925  
 Thr Ser Leu Gly Leu Leu Pro Val Pro Pro Glu Phe Trp Asn Lys Ser  
 930 935 940  
 Met Leu Glu Lys Pro Thr Asp Gly Arg Glu Val Val Cys His Ala Ser  
 945 950 955 960  
 Ala Trp Asp Phe Tyr Asn Gly Lys Asp Phe Arg Ile Lys Gln Cys Thr  
 965 970 975

Thr Val Asn Leu Glu Asp Leu Val Val Ala His His Glu Met Gly His  
 980 985 990  
 Ile Gln Tyr Phe Met Gln Tyr Lys Asp Leu Pro Val Ala Leu Arg Glu  
 995 1000 1005  
 Gly Ala Asn Pro Gly Phe His Glu Ala Ile Gly Asp Val Leu Ala Leu  
 1010 1015 1020  
 Ser Val Ser Thr Pro Lys His Leu His Ser Leu Asn Leu Leu Ser Ser  
 1025 1030 1035 1040  
 Glu Gly Gly Ser Asp Glu His Asp Ile Asn Phe Leu Met Lys Met Ala  
 1045 1050 1055  
 Leu Asp Lys Ile Ala Phe Ile Pro Phe Ser Tyr Leu Val Asp Gln Trp  
 1060 1065 1070  
 Arg Trp Arg Val Phe Asp Gly Ser Ile Thr Lys Glu Asn Tyr Asn Gln  
 1075 1080 1085  
 Glu Trp Trp Ser Leu Arg Leu Lys Tyr Gln Gly Leu Cys Pro Pro Val  
 1090 1095 1100  
 Pro Arg Thr Gln Gly Asp Phe Asp Pro Gly Ala Lys Phe His Ile Pro  
 1105 1110 1115 1120  
 Ser Ser Val Pro Tyr Ile Arg Tyr Phe Val Ser Phe Ile Ile Gln Phe  
 1125 1130 1135  
 Gln Phe His Glu Ala Leu Cys Gln Ala Ala Gly His Thr Gly Pro Leu  
 1140 1145 1150  
 His Lys Cys Asp Ile Tyr Gln Ser Lys Glu Ala Gly Gln Arg Leu Ala  
 1155 1160 1165  
 Thr Ala Met Lys Leu Gly Phe Ser Arg Pro Trp Pro Glu Ala Met Gln  
 1170 1175 1180  
 Leu Ile Thr Gly Gln Pro Asn Met Ser Ala Ser Ala Met Leu Ser Tyr  
 1185 1190 1195 1200  
 Phe Lys Pro Leu Leu Asp Trp Leu Arg Thr Glu Asn Glu Leu His Gly  
 1205 1210 1215  
 Glu Lys Leu Gly Trp Pro Gln Tyr Asn Trp Thr Pro Asn Ser Ala Arg  
 1220 1225 1230  
 Ser Glu Gly Pro Leu Pro Asp Ser Gly Arg Val Ser Phe Leu Gly Leu  
 1235 1240 1245  
 Asp Leu Asp Ala Gln Gln Ala Arg Val Gly Gln Trp Leu Leu Leu Phe  
 1250 1255 1260  
 Leu Gly Ile Ala Leu Leu Val Ala Thr Leu Gly Leu Ser Gln Arg Leu  
 1265 1270 1275 1280  
 Phe Ser Ile Arg His Arg Ser Leu His Arg His Ser His Gly Pro Gln  
 1285 1290 1295

Phe Gly Ser Glu Val Glu Leu Arg His Ser  
                   1300                                  1305

<210> 8

<211> 1312

<212> PRT

<213> Murine sp.

<220>

<223> Description of Artificial Sequence: motifs

<400> 8

Met Gly Ala Ala Ser Gly Gln Arg Gly Arg Trp Pro Leu Ser Pro Pro  
   1                                  5                                  10                                  15

Leu Leu Met Leu Ser Leu Leu Val Leu Leu Leu Gln Pro Ser Pro Ala  
                   20                                  25                                  30

Pro Ala Leu Asp Pro Gly Leu Gln Pro Gly Asn Phe Ser Pro Asp Glu  
                   35                                  40                                  45

Ala Gly Ala Gln Leu Phe Ala Glu Ser Tyr Asn Ser Ser Ala Glu Val  
                   50                                  55                                  60

Val Met Phe Gln Ser Thr Val Ala Ser Trp Ala His Asp Thr Asn Ile  
   65                                  70                                  75                                  80

Thr Glu Glu Asn Ala Arg Arg Gln Glu Glu Ala Ala Leu Val Ser Gln  
                                   85                                  90                                  95

Glu Phe Ala Glu Val Trp Gly Lys Lys Ala Lys Glu Leu Tyr Glu Ser  
                   100                                  105                                  110

Ile Trp Gln Asn Phe Thr Asp Ser Lys Leu Arg Arg Ile Ile Gly Ser  
                   115                                  120                                  125

Ile Arg Thr Leu Gly Pro Ala Asn Leu Pro Leu Ala Gln Arg Gln Gln  
   130                                  135                                  140

Tyr Asn Ser Leu Leu Ser Asn Met Ser Arg Ile Tyr Ser Thr Gly Lys  
   145                                  150                                  155                                  160

Val Cys Phe Pro Asn Lys Thr Ala Thr Cys Trp Ser Leu Asp Pro Glu  
                   165                                  170                                  175

Leu Thr Asn Ile Leu Ala Ser Ser Arg Ser Tyr Ala Lys Leu Leu Phe  
                   180                                  185                                  190

Ala Trp Glu Gly Trp His Asp Ala Val Gly Ile Pro Leu Lys Pro Leu  
                   195                                  200                                  205

Tyr Gln Asp Phe Thr Ala Ile Ser Asn Glu Ala Tyr Arg Gln Asp Asp  
   210                                  215                                  220

Phe Ser Asp Thr Gly Ala Phe Trp Arg Ser Trp Tyr Glu Ser Pro Ser  
   225                                  230                                  235                                  240

Phe Glu Glu Ser Leu Glu His Ile Tyr His Gln Leu Glu Pro Leu Tyr  
                   245                                  250                                  255

Leu Asn Leu His Ala Tyr Val Arg Arg Ala Leu His Arg Arg Tyr Gly  
 260 265 270  
 Asp Lys Tyr Val Asn Leu Arg Gly Pro Ile Pro Ala His Leu Leu Gly  
 275 280 285  
 Asp Met Trp Ala Gln Ser Trp Glu Asn Ile Tyr Asp Met Val Val Pro  
 290 295 300  
 Phe Pro Asp Lys Pro Asn Leu Asp Val Thr Ser Thr Met Val Gln Lys  
 305 310 315 320  
 Gly Trp Asn Ala Thr His Met Phe Arg Val Ser Glu Glu Phe Phe Thr  
 325 330 335  
 Ser Leu Gly Leu Ser Pro Met Pro Pro Glu Phe Trp Ala Glu Ser Met  
 340 345 350  
 Leu Glu Lys Pro Thr Asp Gly Arg Glu Val Val Cys His Ala Ser Ala  
 355 360 365  
 Trp Asp Phe Tyr Asn Arg Lys Asp Phe Arg Ile Lys Gln Cys Thr Arg  
 370 375 380  
 Val Thr Met Glu Gln Leu Ala Thr Val His His Glu Met Gly His Val  
 385 390 395 400  
 Gln Tyr Tyr Leu Gln Tyr Lys Asp Leu His Val Ser Leu Arg Arg Gly  
 405 410 415  
 Ala Asn Pro Gly Phe His Glu Ala Ile Gly Asp Val Leu Ala Leu Ser  
 420 425 430  
 Val Ser Thr Pro Ala His Leu His Lys Ile Gly Leu Leu Asp His Val  
 435 440 445  
 Thr Asn Asp Ile Glu Ser Asp Ile Asn Tyr Leu Leu Lys Met Ala Leu  
 450 455 460  
 Glu Lys Ile Ala Phe Leu Pro Phe Gly Tyr Leu Val Asp Gln Trp Arg  
 465 470 475 480  
 Trp Gly Val Phe Ser Gly Arg Thr Pro Pro Ser Arg Tyr Asn Phe Asp  
 485 490 495  
 Trp Trp Tyr Leu Arg Thr Lys Tyr Gln Gly Ile Cys Pro Pro Val Ala  
 500 505 510  
 Arg Asn Glu Thr His Phe Asp Ala Gly Ala Lys Phe His Ile Pro Asn  
 515 520 525  
 Val Thr Pro Tyr Ile Arg Tyr Phe Val Ser Phe Val Leu Gln Phe Gln  
 530 535 540  
 Phe His Gln Ala Leu Cys Lys Glu Ala Gly His Gln Gly Pro Leu His  
 545 550 555 560  
 Gln Cys Asp Ile Tyr Gln Ser Thr Gln Ala Gly Ala Lys Leu Lys Gln  
 565 570 575

Val Leu Gln Ala Gly Cys Ser Arg Pro Trp Gln Glu Val Leu Lys Asp  
580 585 590

Leu Val Gly Ser Asp Ala Leu Asp Ala Lys Ala Leu Leu Glu Tyr Phe  
595 600 605

Gln Pro Val Ser Gln Trp Leu Glu Glu Gln Asn Gln Arg Asn Gly Glu  
610 615 620

Val Leu Gly Trp Pro Glu Asn Gln Trp Arg Pro Pro Leu Pro Asp Asn  
625 630 635 640

Tyr Pro Glu Gly Ile Asp Leu Glu Thr Asp Glu Ala Lys Ala Asp Arg  
645 650 655

Phe Val Glu Glu Tyr Asp Arg Thr Ala Gln Val Leu Leu Asn Glu Tyr  
660 665 670

Ala Glu Ala Asn Trp Gln Tyr Asn Thr Asn Ile Thr Ile Glu Gly Ser  
675 680 685

Lys Ile Leu Leu Glu Lys Ser Thr Glu Val Ser Asn His Thr Leu Lys  
690 695 700

Tyr Gly Thr Arg Ala Lys Thr Phe Asp Val Ser Asn Phe Gln Asn Ser  
705 710 715 720

Ser Ile Lys Arg Ile Ile Lys Lys Leu Gln Asn Leu Asp Arg Ala Val  
725 730 735

Leu Pro Pro Lys Glu Leu Glu Glu Tyr Asn Gln Ile Leu Leu Asp Met  
740 745 750

Glu Thr Thr Tyr Ser Leu Ser Asn Ile Cys Tyr Thr Asn Gly Thr Cys  
755 760 765

Met Pro Leu Glu Pro Asp Leu Thr Asn Met Met Ala Thr Ser Arg Lys  
770 775 780

Tyr Glu Glu Leu Leu Trp Ala Trp Lys Ser Trp Arg Asp Lys Val Gly  
785 790 795 800

Arg Ala Ile Leu Pro Phe Phe Pro Lys Tyr Val Glu Phe Ser Asn Lys  
805 810 815

Ile Ala Lys Leu Asn Gly Tyr Thr Asp Ala Gly Asp Ser Trp Arg Ser  
820 825 830

Leu Tyr Glu Ser Asp Asn Leu Glu Gln Asp Leu Glu Lys Leu Tyr Gln  
835 840 845

Glu Leu Gln Pro Leu Tyr Leu Asn Leu His Ala Tyr Val Arg Arg Ser  
850 855 860

Leu His Arg His Tyr Gly Ser Glu Tyr Ile Asn Leu Asp Gly Pro Ile  
865 870 875 880

Pro Ala His Leu Leu Gly Asn Met Trp Ala Gln Thr Trp Ser Asn Ile  
885 890 895

Tyr Asp Leu Val Ala Pro Phe Pro Ser Ala Pro Asn Ile Asp Ala Thr  
 900 905 910  
 Glu Ala Met Ile Lys Gln Gly Trp Thr Pro Arg Arg Ile Phe Lys Glu  
 915 920 925  
 Ala Asp Asn Phe Phe Thr Ser Leu Gly Leu Leu Pro Val Pro Pro Glu  
 930 935 940  
 Phe Trp Asn Lys Ser Met Leu Glu Lys Pro Thr Asp Gly Arg Glu Val  
 945 950 955 960  
 Val Cys His Pro Ser Ala Trp Asp Phe Tyr Asn Gly Lys Asp Phe Arg  
 965 970 975  
 Ile Lys Gln Cys Thr Ser Val Asn Met Glu Asp Leu Val Ile Ala His  
 980 985 990  
 His Glu Met Gly His Ile Gln Tyr Phe Met Gln Tyr Lys Asp Leu Pro  
 995 1000 1005  
 Val Thr Phe Arg Glu Gly Ala Asn Pro Gly Phe His Glu Ala Ile Gly  
 1010 1015 1020  
 Asp Ile Met Ala Leu Ser Val Ser Thr Pro Lys His Leu Tyr Ser Leu  
 1025 1030 1035 1040  
 Asn Leu Leu Ser Thr Glu Gly Ser Gly Tyr Glu Tyr Asp Ile Asn Phe  
 1045 1050 1055  
 Leu Met Lys Met Ala Leu Asp Lys Ile Ala Phe Ile Pro Phe Ser Tyr  
 1060 1065 1070  
 Leu Ile Asp Gln Trp Arg Trp Arg Val Phe Asp Gly Ser Ile Thr Lys  
 1075 1080 1085  
 Glu Asn Tyr Asn Gln Glu Trp Trp Ser Leu Arg Leu Lys Tyr Gln Gly  
 1090 1095 1100  
 Leu Cys Pro Pro Val Pro Arg Ser Gln Gly Asp Phe Asp Pro Gly Ser  
 1105 1110 1115 1120  
 Lys Phe His Val Pro Ala Asn Val Pro Tyr Val Arg Tyr Phe Val Ser  
 1125 1130 1135  
 Phe Ile Ile Gln Phe Gln Phe His Glu Ala Leu Cys Arg Ala Ala Gly  
 1140 1145 1150  
 His Thr Gly Pro Leu His Lys Cys Asp Ile Tyr Gln Ser Lys Glu Ala  
 1155 1160 1165  
 Gly Lys Leu Leu Ala Asp Ala Met Lys Leu Gly Tyr Ser Lys Pro Trp  
 1170 1175 1180  
 Pro Glu Ala Met Lys Leu Ile Thr Gly Gln Pro Asn Met Ser Ala Ser  
 1185 1190 1195 1200  
 Ala Met Met Asn Tyr Phe Lys Pro Leu Thr Glu Trp Leu Val Thr Glu  
 1205 1210 1215



Asn Arg Arg His Gly Glu Thr Leu Gly Trp Pro Glu Tyr Asn Trp Ala  
 1220 1225 1230

Pro Asn Thr Ala Arg Ala Glu Gly Ser Thr Ala Glu Ser Asn Arg Val  
 1235 1240 1245

Asn Phe Leu Gly Leu Tyr Leu Glu Pro Gln Gln Ala Arg Val Gly Gln  
 1250 1255 1260

Trp Val Leu Leu Phe Leu Gly Val Ala Leu Leu Val Ala Thr Val Gly  
 1265 1270 1275 1280

Leu Ala His Arg Leu Tyr Asn Ile Arg Asn His His Ser Leu Arg Arg  
 1285 1290 1295

Pro His Arg Gly Pro Gln Phe Gly Ser Glu Val Glu Leu Arg His Ser  
 1300 1305 1310

<210> 9

<211> 1313

<212> PRT

<213> Rattus rattus

<220>

<223> Description of Artificial Sequence: motifs

<400> 9

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Leu Leu Met Leu Ser Leu Leu Leu Leu Leu Leu Pro Pro Ser Pro  
 20 25 30

Ala Pro Ala Leu Asp Pro Gly Leu Gln Pro Gly Asn Phe Ser Ala Asp  
 35 40 45

Glu Ala Gly Ala Gln Leu Phe Ala Asp Ser Tyr Asn Ser Ser Ala Glu  
 50 55 60

Val Val Met Phe Gln Ser Thr Ala Ala Ser Trp Ala His Asp Thr Asn  
 65 70 75 80

Ile Thr Glu Glu Asn Ala Arg Leu Gln Glu Glu Ala Ala Leu Ile Asn  
 85 90 95

Gln Glu Phe Ala Glu Val Trp Gly Lys Lys Ala Lys Glu Leu Tyr Glu  
 100 105 110

Ser Ile Trp Gln Asn Phe Thr Asp Gln Lys Leu Arg Arg Ile Ile Gly  
 115 120 125

Ser Val Gln Thr Leu Gly Pro Ala Asn Leu Pro Leu Thr Gln Arg Leu  
 130 135 140

Gln Tyr Asn Ser Leu Leu Ser Asn Met Ser Arg Ile Tyr Ser Thr Gly  
 145 150 155 160

Lys Val Cys Phe Pro Asn Lys Thr Ala Thr Cys Trp Ser Leu Asp Pro  
 165 170 175  
 Glu Leu Thr Asn Ile Leu Ala Ser Ser Arg Asn Tyr Ala Lys Val Leu  
 180 185 190  
 Phe Ala Trp Glu Gly Trp His Asp Ala Val Gly Ile Pro Leu Arg Pro  
 195 200 205  
 Leu Tyr Gln Asp Phe Thr Ala Leu Ser Asn Glu Ala Tyr Arg Gln Asp  
 210 215 220  
 Gly Phe Ser Asp Thr Gly Ala Tyr Trp Arg Ser Trp Tyr Glu Ser Pro  
 225 230 235 240  
 Ser Phe Glu Glu Ser Leu Glu His Leu Tyr His Gln Val Glu Pro Leu  
 245 250 255  
 Tyr Leu Asn Leu His Ala Phe Val Arg Arg Ala Leu His Arg Arg Tyr  
 260 265 270  
 Gly Asp Lys Tyr Ile Asn Leu Arg Gly Pro Ile Pro Ala His Leu Leu  
 275 280 285  
 Gly Asp Met Trp Ala Gln Ser Trp Glu Asn Ile Tyr Asp Met Val Val  
 290 295 300  
 Pro Phe Pro Asp Lys Pro Asn Leu Asp Val Thr Ser Thr Met Val Gln  
 305 310 315 320  
 Lys Gly Trp Asn Ala Thr His Met Phe Arg Val Ala Glu Glu Phe Phe  
 325 330 335  
 Thr Ser Leu Gly Leu Ser Pro Met Pro Pro Glu Phe Trp Ala Glu Ser  
 340 345 350  
 Met Leu Glu Lys Pro Ala Asp Gly Arg Glu Val Val Cys His Ala Ser  
 355 360 365  
 Ala Trp Asp Phe Tyr Asn Arg Lys Asp Phe Arg Ile Lys Gln Cys Thr  
 370 375 380  
 Arg Val Thr Met Asp Gln Leu Ser Thr Val His His Glu Met Gly His  
 385 390 395 400  
 Val Gln Tyr Tyr Leu Gln Tyr Lys Asp Leu His Val Ser Leu Arg Arg  
 405 410 415  
 Gly Ala Asn Pro Gly Phe His Glu Ala Ile Gly Asp Val Leu Ala Leu  
 420 425 430  
 Ser Val Ser Thr Pro Ala His Leu His Lys Ile Gly Leu Leu Asp Arg  
 435 440 445  
 Val Ala Asn Asp Ile Glu Ser Asp Ile Asn Tyr Leu Leu Lys Met Ala  
 450 455 460  
 Leu Glu Lys Ile Ala Phe Leu Pro Phe Gly Tyr Leu Val Asp Gln Trp  
 465 470 475 480

Arg Trp Gly Val Phe Ser Gly Arg Thr Pro Pro Ser Arg Tyr Asn Tyr  
 485 490 495  
 Asp Trp Trp Tyr Leu Arg Thr Lys Tyr Gln Gly Ile Cys Pro Pro Val  
 500 505 510  
 Ala Arg Asn Glu Thr His Phe Asp Ala Gly Ala Lys Phe His Ile Pro  
 515 520 525  
 Ser Val Thr Pro Tyr Ile Arg Tyr Phe Val Ser Phe Val Leu Gln Phe  
 530 535 540  
 Gln Phe His Gln Ala Leu Cys Lys Glu Ala Gly His Gln Gly Pro Leu  
 545 550 555 560  
 His Gln Cys Asp Ile Tyr Gln Ser Thr Lys Ala Gly Ala Lys Leu Gln  
 565 570 575  
 Gln Val Leu Gln Ala Gly Cys Ser Arg Pro Trp Gln Glu Val Leu Lys  
 580 585 590  
 Asp Leu Val Gly Ser Asp Ala Leu Asp Ala Ser Ala Leu Met Glu Tyr  
 595 600 605  
 Phe Gln Pro Val Ser Gln Trp Leu Gln Glu Gln Asn Gln Arg Asn Gly  
 610 615 620  
 Glu Val Leu Gly Trp Pro Glu Tyr Gln Trp Arg Pro Pro Leu Pro Asp  
 625 630 635 640  
 Asn Tyr Pro Glu Gly Ile Asp Leu Glu Thr Asp Glu Ala Lys Ala Asn  
 645 650 655  
 Arg Phe Val Glu Glu Tyr Asp Arg Thr Ala Lys Val Leu Trp Asn Glu  
 660 665 670  
 Tyr Ala Glu Ala Asn Trp His Tyr Asn Thr Asn Ile Thr Ile Glu Gly  
 675 680 685  
 Ser Lys Ile Leu Leu Gln Lys Asn Lys Glu Val Ser Asn His Thr Leu  
 690 695 700  
 Lys Tyr Gly Thr Trp Ala Lys Thr Phe Asp Val Ser Asn Phe Gln Asn  
 705 710 715 720  
 Ser Thr Ile Lys Arg Ile Ile Lys Lys Val Gln Asn Val Asp Arg Ala  
 725 730 735  
 Val Leu Pro Pro Asn Glu Leu Glu Glu Tyr Asn Gln Ile Leu Leu Asp  
 740 745 750  
 Met Glu Thr Thr Tyr Ser Val Ala Asn Val Cys Tyr Thr Asn Gly Thr  
 755 760 765  
 Cys Leu Ser Leu Glu Pro Asp Leu Thr Asn Ile Met Ala Thr Ser Arg  
 770 775 780  
 Lys Tyr Glu Glu Leu Leu Trp Val Trp Lys Ser Trp Arg Asp Lys Val  
 785 790 795 800

Gly	Arg	Ala	Ile	Leu	Pro	Phe	Phe	Pro	Lys	Tyr	Val	Asp	Phe	Ser	Asn
				805						810		815			
Lys	Ile	Ala	Lys	Leu	Asn	Gly	Tyr	Ser	Asp	Ala	Gly	Asp	Ser	Trp	Arg
				820						825		830			
Ser	Ser	Tyr	Glu	Ser	Asp	Asp	Leu	Glu	Gln	Asp	Leu	Glu	Lys	Leu	Tyr
				835						840		845			
Gln	Glu	Leu	Gln	Pro	Leu	Tyr	Leu	Asn	Leu	His	Ala	Tyr	Val	Arg	Arg
				850						855		860			
Ser	Leu	His	Arg	His	Tyr	Gly	Ser	Glu	Tyr	Ile	Asn	Leu	Asp	Gly	Pro
				865						870		875			
Ile	Pro	Ala	His	Leu	Leu	Gly	Asn	Met	Trp	Ala	Gln	Thr	Trp	Ser	Asn
				885						890		895			
Ile	Tyr	Asp	Leu	Val	Ala	Pro	Phe	Pro	Ser	Ala	Pro	Ser	Ile	Asp	Ala
				900						905		910			
Thr	Glu	Ala	Met	Ile	Lys	Gln	Gly	Trp	Thr	Pro	Arg	Arg	Ile	Phe	Lys
				915						920		925			
Glu	Ala	Asp	Asn	Phe	Phe	Thr	Ser	Leu	Gly	Leu	Leu	Pro	Val	Pro	Pro
				930						935		940			
Glu	Phe	Trp	Asn	Lys	Ser	Met	Leu	Glu	Lys	Pro	Thr	Asp	Gly	Arg	Glu
				945						950		955			
Val	Val	Cys	His	Ala	Ser	Ala	Trp	Asp	Phe	Tyr	Asn	Gly	Lys	Asp	Phe
				965						970		975			
Arg	Ile	Lys	Gln	Cys	Thr	Ser	Val	Asn	Met	Glu	Glu	Leu	Val	Ile	Ala
				980						985		990			
His	His	Glu	Met	Gly	His	Ile	Gln	Tyr	Phe	Met	Gln	Tyr	Lys	Asp	Leu
				995						1000		1005			
Pro	Val	Thr	Phe	Arg	Glu	Gly	Ala	Asn	Pro	Gly	Phe	His	Glu	Ala	Ile
				1010						1015		1020			
Gly	Asp	Val	Leu	Ala	Leu	Ser	Val	Ser	Thr	Pro	Lys	His	Leu	His	Ser
				1025						1030		1035			
Leu	Asn	Leu	Leu	Ser	Ser	Glu	Gly	Ser	Gly	Tyr	Glu	His	Asp	Ile	Asn
				1045						1050		1055			
Phe	Leu	Met	Lys	Met	Ala	Leu	Asp	Lys	Ile	Ala	Phe	Ile	Pro	Phe	Ser
				1060						1065		1070			
Tyr	Leu	Ile	Asp	Gln	Trp	Arg	Trp	Arg	Val	Phe	Asp	Gly	Ser	Ile	Thr
				1075						1080		1085			
Lys	Glu	Asn	Tyr	Asn	Gln	Glu	Trp	Trp	Ser	Leu	Arg	Leu	Lys	Tyr	Gln
				1090						1095		1100			
Gly	Leu	Cys	Pro	Pro	Val	Pro	Arg	Ser	Gln	Gly	Asp	Phe	Asp	Pro	Gly
				1105						1110		1115			
												1120			

Ala Gly Ala Arg Leu Phe Ala Ser Ser Tyr Asn Ser Ser Ala Glu Gln  
50 55 60

Val Leu Phe Arg Ser Thr Ala Ala Ser Trp Ala His Asp Thr Asn Ile  
 65 70 75 80  
 Thr Ala Glu Asn Ala Arg Arg Gln Glu Glu Glu Ala Leu Leu Ser Gln  
 85 90 95  
 Glu Phe Ala Glu Ala Trp Gly Lys Lys Ala Lys Glu Leu Tyr Asp Pro  
 100 105 110  
 Val Trp Gln Asn Phe Thr Asp Pro Glu Leu Arg Arg Ile Ile Gly Ala  
 115 120 125  
 Val Arg Thr Leu Gly Pro Ala Asn Leu Pro Leu Ala Lys Arg Gln Gln  
 130 135 140  
 Tyr Asn Ser Leu Leu Ser Asn Met Ser Gln Ile Tyr Ser Thr Gly Lys  
 145 150 155 160  
 Val Cys Phe Pro Asn Lys Thr Ala Ser Cys Trp Ser Leu Asp Pro Asp  
 165 170 175  
 Leu Asn Asn Ile Leu Ala Ser Ser Arg Ser Tyr Ala Met Leu Leu Phe  
 180 185 190  
 Ala Trp Glu Gly Trp His Asn Ala Val Gly Ile Pro Leu Lys Pro Leu  
 195 200 205  
 Tyr Gln Glu Phe Thr Ala Leu Ser Asn Glu Ala Tyr Arg Gln Asp Gly  
 210 215 220  
 Phe Ser Asp Thr Gly Ala Tyr Trp Arg Ser Trp Tyr Asp Ser Pro Thr  
 225 230 235 240  
 Phe Glu Glu Asp Leu Glu Arg Ile Tyr His Gln Leu Glu Pro Leu Tyr  
 245 250 255  
 Leu Asn Leu His Ala Tyr Val Arg Arg Val Leu His Arg Arg Tyr Gly  
 260 265 270  
 Asp Arg Tyr Ile Asn Leu Arg Gly Pro Ile Pro Ala His Leu Leu Gly  
 275 280 285  
 Asn Met Trp Ala Gln Ser Trp Glu Ser Ile Tyr Asp Met Val Val Pro  
 290 295 300  
 Phe Pro Asp Lys Pro Asn Leu Asp Val Thr Ser Thr Met Val Gln Lys  
 305 310 315 320  
 Gly Trp Asn Ala Thr His Met Phe Arg Val Ala Glu Glu Phe Phe Thr  
 325 330 335  
 Ser Leu Gly Leu Leu Pro Met Pro Pro Glu Phe Trp Ala Glu Ser Met  
 340 345 350  
 Leu Glu Lys Pro Glu Asp Gly Arg Glu Val Val Cys His Ala Ser Ala  
 355 360 365  
 Trp Asp Phe Tyr Asn Arg Lys Asp Phe Arg Ile Lys Gln Cys Thr Gln  
 370 375 380

Val Thr Met Asp Gln Leu Ser Thr Val His His Glu Met Gly His Val  
 385 390 395 400  
 Gln Tyr Tyr Leu Gln Tyr Lys Asp Gln Pro Val Ser Leu Arg Arg Ala  
 405 410 415  
 Asn Pro Gly Phe His Glu Ala Ile Gly Asp Val Leu Ala Leu Ser Val  
 420 425 430  
 Ser Thr Pro Ala His Leu His Lys Ile Gly Leu Leu Asp His Val Thr  
 435 440 445  
 Asn Asp Thr Glu Ser Asp Ile Asn Tyr Leu Leu Lys Met Ala Leu Glu  
 450 455 460  
 Lys Ile Ala Phe Leu Pro Phe Gly Tyr Leu Val Asp Gln Trp Arg Trp  
 465 470 475 480  
 Gly Val Phe Ser Gly Arg Thr Pro Ser Ser Arg Tyr Asn Phe Asp Trp  
 485 490 495  
 Trp Tyr Leu Arg Thr Lys Tyr Gln Gly Ile Cys Pro Pro Val Val Arg  
 500 505 510  
 Asn Glu Thr His Phe Asp Ala Gly Ala Lys Phe His Ile Pro Ser Val  
 515 520 525  
 Thr Pro Tyr Ile Arg Tyr Phe Val Ser Phe Val Leu Gln Phe Gln Phe  
 530 535 540  
 His Gln Ala Leu Cys Met Glu Ala Gly His Gln Gly Pro Leu His Gln  
 545 550 555 560  
 Cys Asp Ile Tyr Gln Ser Thr Arg Ala Gly Ala Lys Leu Arg Ala Val  
 565 570 575  
 Leu Gln Ala Gly Cys Ser Arg Pro Trp Gln Glu Val Leu Lys Asp Met  
 580 585 590  
 Val Ala Ser Asp Ala Leu Asp Ala Gln Pro Leu Leu Asp Tyr Phe Gln  
 595 600 605  
 Pro Val Thr Gln Trp Leu Gln Glu Gln Asn Glu Arg Asn Gly Glu Val  
 610 615 620  
 Leu Gly Trp Pro Glu Tyr Gln Trp Arg Pro Pro Leu Pro Asn Asn Tyr  
 625 630 635 640  
 Pro Glu Gly Ile Asp Leu Val Thr Asp Glu Ala Glu Ala Ser Arg Phe  
 645 650 655  
 Val Glu Glu Tyr Asp Arg Ser Phe Gln Ala Val Trp Asn Glu Tyr Ala  
 660 665 670  
 Glu Ala Asn Trp Asn Tyr Asn Thr Asn Ile Thr Thr Glu Ala Ser Lys  
 675 680 685  
 Ile Leu Leu Gln Lys Asn Met Gln Ile Ala Asn His Thr Leu Thr Tyr  
 690 695 700

Gly Asn Trp Ala Arg Arg Phe Asp Val Ser Asn Phe Gln Asn Ala Thr  
 705 710 715 720  
 Ser Lys Arg Ile Ile Lys Lys Val Gln Asp Leu Gln Arg Ala Val Leu  
 725 730 735  
 Pro Val Lys Glu Leu Glu Glu Tyr Asn Gln Ile Leu Leu Asp Met Glu  
 740 745 750  
 Thr Ile Tyr Ser Val Ala Asn Val Cys Arg Val Asp Gly Ser Cys Leu  
 755 760 765  
 Gln Leu Glu Pro Asp Leu Thr Asn Leu Met Ala Thr Ser Arg Lys Tyr  
 770 775 780  
 Asp Glu Leu Leu Trp Val Trp Thr Ser Trp Arg Asp Lys Val Gly Arg  
 785 790 795 800  
 Ala Ile Leu Pro Tyr Phe Pro Lys Tyr Val Glu Phe Thr Asn Lys Ala  
 805 810 815  
 Ala Arg Leu Asn Gly Tyr Val Asp Ala Gly Asp Ser Trp Arg Ser Met  
 820 825 830  
 Tyr Glu Thr Pro Thr Leu Glu Gln Asp Leu Glu Arg Leu Phe Gln Glu  
 835 840 845  
 Leu Gln Pro Leu Tyr Leu Asn Leu His Ala Tyr Val Gly Arg Ala Leu  
 850 855 860  
 His Arg His Tyr Gly Ala Gln His Ile Asn Leu Glu Gly Pro Ile Pro  
 865 870 875 880  
 Ala His Leu Leu Gly Asn Met Trp Ala Gln Thr Trp Ser Asn Ile Tyr  
 885 890 895  
 Asp Leu Val Ala Pro Phe Pro Ser Ala Ser Thr Met Asp Ala Thr Glu  
 900 905 910  
 Ala Met Ile Lys Gln Gly Trp Thr Pro Arg Arg Met Phe Glu Glu Ala  
 915 920 925  
 Asp Lys Phe Phe Ile Ser Leu Gly Leu Leu Pro Val Pro Pro Glu Phe  
 930 935 940  
 Trp Asn Lys Ser Met Leu Glu Lys Pro Thr Asp Gly Arg Glu Val Val  
 945 950 955 960  
 Cys His Ala Ser Ala Trp Asp Phe Tyr Asn Gly Lys Asp Phe Arg Ile  
 965 970 975  
 Lys Gln Cys Thr Thr Val Asn Met Glu Asp Leu Val Val Val His His  
 980 985 990  
 Glu Met Gly His Ile Gln Tyr Phe Met Gln Tyr Lys Asp Leu Pro Val  
 995 1000 1005  
 Ala Leu Arg Glu Gly Ala Asn Pro Gly Phe His Glu Ala Ile Gly Asp  
 1010 1015 1020



Val Leu Ala Leu Ser Val Ser Thr Pro Lys His Leu His Ser Ile Asn  
 1025 1030 1035 1040  
 Leu Leu Ser Ser Glu Gly Gly Gly Tyr Glu His Asp Ile Asn Phe Leu  
 1045 1050 1055  
 Met Lys Met Ala Leu Asp Lys Ile Ala Phe Ile Pro Phe Ser Tyr Leu  
 1060 1065 1070  
 Val Asp Glu Trp Arg Trp Arg Val Phe Asp Gly Ser Ile Thr Lys Glu  
 1075 1080 1085  
 Asn Tyr Asn Gln Glu Trp Trp Ser Leu Arg Leu Lys Tyr Gln Gly Leu  
 1090 1095 1100  
 Cys Pro Pro Ala Pro Arg Ser Gln Gly Asp Phe Asp Pro Gly Ala Lys  
 1105 1110 1115 1120  
 Phe His Ile Pro Ser Ser Val Pro Tyr Ile Arg Tyr Phe Val Ser Phe  
 1125 1130 1135  
 Ile Ile Gln Phe Gln Phe His Glu Ala Leu Cys Lys Ala Ala Gly His  
 1140 1145 1150  
 Thr Gly Pro Leu His Thr Cys Asp Ile Tyr Gln Ser Lys Glu Ala Gly  
 1155 1160 1165  
 Lys Arg Leu Ala Asp Ala Met Lys Leu Gly Tyr Ser Lys Pro Trp Pro  
 1170 1175 1180  
 Glu Ala Met Lys Val Ile Thr Gly Gln Pro Asn Met Ser Ala Ser Ala  
 1185 1190 1195 1200  
 Met Met Asn Tyr Phe Lys Pro Leu Met Asp Trp Leu Leu Thr Glu Asn  
 1205 1210 1215  
 Gly Arg His Gly Glu Lys Leu Gly Trp Pro Gln Tyr Thr Trp Thr Pro  
 1220 1225 1230  
 Asn Ser Ala Arg Ser Glu Gly Ser Leu Pro Asp Ser Gly Arg Val Asn  
 1235 1240 1245  
 Phe Leu Gly Met Asn Leu Asp Ala Gln Gln Ala Arg Val Gly Gln Trp  
 1250 1255 1260  
 Val Leu Leu Phe Leu Gly Val Ala Leu Leu Leu Ala Ser Leu Gly Leu  
 1265 1270 1275 1280  
 Thr Gln Arg Leu Phe Ser Ile Arg Tyr Gln Ser Leu Arg Gln Pro His  
 1285 1290 1295  
 His Gly Pro Gln Phe Gly Ser Glu Val Glu Leu Arg His Ser  
 1300 1305 1310

<210> 11  
 <211> 615  
 <212> PRT  
 <213> *Drosophila melanogaster*  
 <220>

## &lt;223&gt; Description of Artificial Sequence: motifs

&lt;400&gt; 11

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Met Arg Leu Phe Leu Leu Ala Leu Leu Ala Thr Leu Ala Val Thr Gln
 1           5           10           15

Ala Leu Val Lys Glu Glu Ile Gln Ala Lys Glu Tyr Leu Glu Asn Leu
      20           25           30

Asn Lys Glu Leu Ala Lys Arg Thr Asn Val Glu Thr Glu Ala Ala Trp
      35           40           45

Ala Tyr Gly Ser Asn Ile Thr Asp Glu Asn Glu Lys Lys Lys Asn Glu
      50           55           60

Ile Ser Ala Glu Leu Ala Lys Phe Met Lys Glu Val Ala Ser Asp Thr
      65           70           75           80

Thr Lys Phe Gln Trp Arg Ser Tyr Gln Ser Glu Asp Leu Lys Arg Gln
      85           90           95

Phe Lys Ala Leu Thr Lys Leu Gly Tyr Ala Ala Leu Pro Glu Asp Asp
      100          105          110

Tyr Ala Glu Leu Leu Asp Thr Leu Ser Ala Met Glu Ser Asn Phe Ala
      115          120          125

Lys Val Lys Val Cys Asp Tyr Lys Asp Ser Thr Lys Cys Asp Leu Ala
      130          135          140

Leu Asp Pro Glu Ile Glu Glu Val Ile Ser Lys Ser Arg Asp His Glu
      145          150          155          160

Glu Leu Ala Tyr Tyr Trp Arg Glu Phe Tyr Asp Lys Ala Gly Thr Ala
      165          170          175

Val Arg Ser Gln Phe Glu Arg Tyr Val Glu Leu Asn Thr Lys Ala Ala
      180          185          190

Lys Leu Asn Asn Phe Thr Ser Gly Ala Glu Ala Trp Leu Asp Glu Tyr
      195          200          205

Glu Asp Asp Thr Phe Glu Gln Gln Leu Glu Asp Ile Phe Ala Asp Ile
      210          215          220

Arg Pro Leu Tyr Gln Gln Ile His Gly Tyr Val Arg Phe Arg Leu Arg
      225          230          235          240

Lys His Tyr Gly Asp Ala Val Val Ser Glu Thr Gly Pro Ile Pro Met
      245          250          255

His Leu Leu Gly Asn Met Trp Ala Gln Gln Trp Ser Glu Ile Ala Asp
      260          265          270

Ile Val Ser Pro Phe Pro Glu Lys Pro Leu Val Asp Val Ser Ala Glu
      275          280          285

Met Glu Lys Gln Ala Tyr Thr Pro Leu Lys Met Phe Gln Met Gly Asp
      290          295          300

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Asp Phe Phe Thr Ser Met Asn Leu Thr Lys Leu Pro Gln Asp Phe Trp  
 305 310 315 320  
 Asp Lys Ser Ile Ile Glu Lys Pro Thr Asp Gly Arg Asp Leu Val Cys  
 325 330 335  
 His Ala Ser Ala Trp Asp Phe Tyr Leu Ile Asp Asp Val Arg Ile Lys  
 340 345 350  
 Gln Cys Thr Arg Val Thr Gln Asp Gln Leu Phe Thr Val His His Glu  
 355 360 365  
 Leu Gly His Ile Gln Tyr Phe Leu Gln Tyr Gln His Gln Pro Phe Val  
 370 375 380  
 Tyr Arg Thr Gly Ala Asn Pro Gly Phe His Glu Ala Val Gly Asp Val  
 385 390 395 400  
 Leu Ser Leu Ser Val Ser Thr Pro Lys His Leu Glu Lys Ile Gly Leu  
 405 410 415  
 Leu Lys Asp Tyr Val Arg Asp Asp Glu Ala Arg Ile Asn Gln Leu Phe  
 420 425 430  
 Leu Thr Ala Leu Asp Lys Ile Val Phe Leu Pro Phe Ala Phe Thr Met  
 435 440 445  
 Asp Lys Tyr Arg Trp Ser Leu Phe Arg Gly Glu Val Asp Lys Ala Asn  
 450 455 460  
 Trp Asn Cys Ala Phe Trp Lys Leu Arg Asp Glu Tyr Ser Gly Ile Glu  
 465 470 475 480  
 Pro Pro Val Val Arg Ser Glu Lys Asp Phe Asp Ala Pro Ala Lys Tyr  
 485 490 495  
 His Ile Ser Ala Asp Val Glu Tyr Leu Arg Tyr Leu Val Ser Phe Ile  
 500 505 510  
 Ile Gln Phe Gln Phe Tyr Lys Ser Ala Cys Ile Lys Ala Gly Gln Tyr  
 515 520 525  
 Asp Pro Asp Asn Val Glu Leu Pro Leu Asp Asn Cys Asp Ile Tyr Gly  
 530 535 540  
 Ser Ala Arg Ala Gly Ala Ala Phe His Asn Met Leu Ser Met Gly Ala  
 545 550 555 560  
 Ser Lys Pro Trp Pro Asp Ala Leu Glu Ala Phe Asn Gly Glu Arg Ile  
 565 570 575  
 Met Ser Gly Lys Ala Ile Ala Glu Tyr Phe Glu Pro Leu Arg Val Trp  
 580 585 590  
 Leu Glu Ala Glu Asn Ile Lys Asn Asn Val His Ile Gly Trp Thr Thr  
 595 600 605  
 Ser Asn Lys Cys Val Ser Ser  
 610 615

<210> 12  
 <211> 907  
 <212> PRT  
 <213> Caenorhabditis elegans

<220>

<223> Description of Artificial Sequence: motifs

<400> 12

Met	Lys	Phe	His	Ile	Leu	Leu	Leu	Leu	Leu	Val	Gly	Ala	Cys	Leu	Pro	1	5	10	15
Val	Phe	Thr	Gln	Glu	Ile	Lys	Pro	Lys	Pro	Glu	Leu	Leu	Pro	Ala	Asp	20	25	30	
Glu	Ala	Pro	Lys	Asp	Pro	Glu	Ala	Val	Phe	Ser	Glu	Gly	Glu	Pro	Phe	35	40	45	
Glu	Leu	Thr	Asp	Ala	Leu	Asp	Thr	Pro	Lys	Asn	Gly	Ser	Val	Pro	Val	50	55	60	
Pro	Glu	Pro	Glu	Pro	Lys	Pro	Glu	Pro	Glu	Pro	Glu	Pro	Glu	Pro	Lys	65	70	75	80
Pro	Glu	Pro	Glu	Pro	Ser	Pro	Thr	Pro	Glu	Pro	Glu	Pro	Ala	Ile	Lys	85	90	95	
Phe	Asp	Asn	Ile	Glu	Ser	Glu	Asp	Tyr	Gly	Asp	Val	Ala	Glu	Thr	Ala	100	105	110	
Ala	Ser	Thr	Gln	Pro	Asp	Glu	Leu	Asn	Thr	Glu	Val	Ile	Glu	Gln	Leu	115	120	125	
Val	Asp	Thr	Phe	Leu	Asn	Thr	Gly	Ser	Ile	Ala	Ser	Asn	Lys	Thr	Asn	130	135	140	
Lys	Gly	Pro	Val	Phe	Ala	Asn	Pro	Val	Ala	Gln	Ala	Leu	Val	Asn	Ser	145	150	155	160
Ser	Asn	Tyr	Trp	Lys	Thr	Asp	Asn	Leu	Gln	Ala	Pro	Gly	Ser	Ile	Lys	165	170	175	
Asp	Glu	Glu	Lys	Leu	Arg	Ser	Trp	Leu	Ala	Gly	Tyr	Glu	Ala	Glu	Ala	180	185	190	
Ile	Lys	Val	Leu	Arg	Glu	Val	Ala	Leu	Ser	Gly	Trp	Arg	Tyr	Phe	Asn	195	200	205	
Asp	Ala	Ser	Pro	Ser	Leu	Lys	Leu	Ala	Leu	Asp	Glu	Ala	Glu	Asn	Val	210	215	220	
Leu	Thr	Met	Phe	Val	Arg	Ser	Thr	Ser	Met	Gln	Ala	Lys	Gln	Phe	Asp	225	230	235	240
Met	Ala	Ser	Val	Thr	Asp	Glu	Lys	Val	Met	Arg	Gln	Leu	Gly	Tyr	Val	245	250	255	
Ser	Phe	Glu	Gly	Met	Ser	Ala	Leu	Ala	Pro	Ser	Arg	Phe	Ala	Asp	Tyr	260	265	270	

Ser Gln Ala Gln Ala Ala Leu Asn Arg Asp Ser Lys Asp Ser Thr Ile  
 275 280 285

Cys Asp Lys Asp Val Pro Pro Pro Cys Ala Leu Gln Lys Ile Asp Met  
 290 295 300

Asp Ser Ile Phe Arg Asn Glu Lys Asp Ala Ser Arg Leu Gln His Leu  
 305 310 315 320

Trp Val Ser Tyr Val Thr Ala Ile Ala Lys Ser Lys Pro Ser Tyr Asn  
 325 330 335

Asn Ile Ile Thr Ile Ser Asn Glu Gly Ala Lys Leu Asn Gly Phe Ala  
 340 345 350

Asn Gly Gly Ala Met Trp Arg Ser Ala Phe Asp Met Ser Ser Lys Val  
 355 360 365

His Lys Ala Glu Phe Asp Leu Asn Lys Gln Ile Asp Lys Ile Tyr Ser  
 370 375 380

Thr Ile Gln Pro Phe Tyr Gln Leu Leu His Ala Tyr Met Arg Arg Gln  
 385 390 395 400

Leu Ala Gly Ile Tyr Ser Asn Pro Val Gly Leu Ser Lys Asp Gly Pro  
 405 410 415

Ile Pro Ala His Leu Phe Gly Ser Leu Asp Gly Gly Asp Trp Ser Ala  
 420 425 430

His Tyr Glu Gln Thr Lys Pro Phe Glu Glu Glu Ser Glu Thr Pro Glu  
 435 440 445

Ala Met Leu Ser Ala Phe Asn Thr Gln Asn Tyr Thr Thr Lys Lys Met  
 450 455 460

Phe Val Thr Ala Tyr Arg Tyr Phe Lys Ser Ala Gly Phe Pro His Leu  
 465 470 475 480

Pro Lys Ser Tyr Trp Thr Ser Ser Ile Phe Ala Arg Val Trp Ser Lys  
 485 490 495

Asp Met Ile Cys His Pro Ala Ala Ala Leu Asp Met Arg Ala Pro Asn  
 500 505 510

Asp Phe Arg Val Lys Ala Cys Ala Gln Leu Gly Glu Pro Asp Phe Glu  
 515 520 525

Gln Ala His Ser Leu Leu Val Gln Thr Tyr Tyr Gln Tyr Leu Tyr Lys  
 530 535 540

Asp Gln Ser Leu Leu Phe Arg Glu Gln Ala Ser Pro Val Ile Thr Asp  
 545 550 555 560

Ala Ile Ala Asn Ala Phe Ala His Leu Ser Thr Asn Pro His Tyr Leu  
 565 570 575

Tyr Ser Gln Lys Leu Val Pro Ser Glu His Leu Asp Ile Lys Asp Ser  
 580 585 590

Val Ile Ile Asn Lys Leu Tyr Lys Glu Ser Leu Glu Ser Phe Thr Lys  
595 600 605

Leu Pro Phe Thr Ile Ala Ala Asp Asn Trp Arg Tyr Glu Leu Phe Asp  
610 615 620

Gly Thr Val Pro Lys Asn Lys Leu Asn Asp Arg Trp Trp Glu Ile Arg  
625 630 635 640

Asn Lys Tyr Glu Gly Val Arg Ser Pro Gln Pro Tyr Asn Thr Ser Asn  
645 650 655

Leu Asp Ala Leu Ile His Asn Ser Val Ser Gln Val His Ser Pro Ala  
660 665 670

Thr Arg Thr Leu Ile Ser Tyr Val Leu Lys Phe Gln Ile Leu Lys Ala  
675 680 685

Leu Cys Gln Arg Glu Leu Phe Trp Leu Ser Glu Gly Cys Ile Leu Ser  
690 695 700

Glu Asp Thr Thr Glu Lys Leu Arg Glu Thr Met Lys Leu Gly Ser Ser  
705 710 715 720

Ile Thr Trp Leu Lys Ala Leu Glu Met Ile Ser Gly Lys Gly Glu Leu  
725 730 735

Asp Ala Gln Pro Leu Leu Glu Tyr Tyr Glu Pro Leu Ile Asn Trp Leu  
740 745 750

Arg Asn Thr Asn Glu Ile Asp Gln Val Val Val Gly Trp Asp Gly Glu  
755 760 765

Gly Thr Pro Phe Thr Val Glu Glu Ile Pro Lys Thr Arg Gln Pro Gly  
770 775 780

Asp Gly Gly Asn Gly Leu Pro Ser Glu Asp Arg Val Ala Phe Pro Gly  
785 790 795 800

Gly Glu Cys Val Asn Gly Gln Glu Cys Leu Leu Asp Ser His Cys Asn  
805 810 815

Gly Thr Ile Cys Val Cys Asn Asp Gly Leu Tyr Thr Leu Glu Ile Gly  
820 825 830

Asn Thr Phe Asn Cys Val Pro Gly Asn Pro Ala Asp Ser Gly Phe Gly  
835 840 845

Asp Gly Lys Gly Gly Leu Val Ile Gly Leu Phe Asn Asn Glu Val Thr  
850 855 860

Thr Pro Glu Pro Ser Ala Glu Pro Glu Pro Thr Ala Lys Thr Thr Thr  
865 870 875 880

Lys Met Pro Pro Arg Val Arg Ala Ala Thr Ser Pro Phe Ser Leu Tyr  
885 890 895

Leu Thr Val Leu Leu Ile Ile Tyr Phe Ala Leu  
900 905

<210> 13  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: motifs

<400> 13  
cacaggttcc accaccccaa ctatctc

27

<210> 14  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: motifs

<400> 14  
His His Glu Met Gly His  
1 5

<210> 15  
<211> 10  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: motifs

<400> 15  
Asp Arg Val Tyr Ile His Pro Phe His Leu  
1 5 10

<210> 16  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: motifs

<400> 16  
Asp Arg Val Tyr Ile His Pro Phe His  
1 5

<210> 17  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: motifs

<400> 17  
Asp Arg Val Tyr Ile His Pro Phe  
1 5

<210> 18  
<211> 7  
<212> PRT  
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<220>  
<223> Description of Artificial Sequence: motifs

<400> 18  
Asp Arg Val Tyr Ile His Pro  
1 5

<210> 19  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: motifs

<400> 19  
Asp Arg Val Tyr Ile His  
1 5

<210> 20  
<211> 5  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: motifs

<400> 20  
Asp Arg Val Tyr Ile  
1 5

<210> 21  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: motifs

<400> 21  
Arg Val Tyr Ile His Pro Phe His Leu  
1 5

<210> 22  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: motifs



<400> 22  
Arg Val Tyr Ile His Pro Phe  
1 5

<210> 23  
<211> 10  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: motifs

<400> 23  
Lys Ile Asn Glu Thr Glu Asn Ser Ile Asn  
1 5 10

<210> 24  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: motifs

<400> 24  
Ile Ala Arg Arg His Pro Tyr Phe  
1 5

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